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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=4; day=15; hr=15; min=37; sec=0; ms=546; ]

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\*\*\*\*\*

Reviewer Comments:

<160> 26

The number provided for numeric identifier <160> must match the total number of sequences in the file. There were 28 sequences counted in this sequence listing. Numeric identifier <160> states there are a total of 26 sequences. Please make all necessary changes.

<210> 27

<211> 20

<212> DNA

<213> homo sapien

<400> 27

atcgacaagg tacccaggat

The sequence rules require that "the enumeration of nucleotide bases shall start at the first base of the sequence with 1. The enumeration shall be continuous through the whole sequence in the direction 5' to 3'. The enumeration shall be marked in the right margin, next to the line containing the one-letter codes for bases, and giving the number of the last base of that line." The enumeration is not marked in the right margin for SEQ ID # 27 and 28, please make all necessary changes.

Numeric Identifier <213> response should be corrected the first letter should be upper case as below:

<213> Homo Sapien

To correct the sequence listing errors noted in this report - The recommended method for correction of errors is to access the sequence listing working file using the software program in which the listing was originally prepared, e.g., the project file in Patent In, make any necessary corrections within that program, then generate a new sequence listing file. Use of a word processing program to correct errors directly in the original sequence listing file is strongly discouraged, since such programs often introduce unintended changes to the sequence listing, rendering the listing unacceptable. When the working file or original program is not available for correction, then use of a common or plain text-only editor, such as NotePad, to edit the original sequence listing file may suffice.

\*\*\*\*\*

Application No: 10574182 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2011-04-06 19:48:13.071  
**Finished:** 2011-04-06 19:48:15.124  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 53 ms  
**Total Warnings:** 28  
**Total Errors:** 3  
**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 28

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2011-04-06 19:48:13.071  
**Finished:** 2011-04-06 19:48:15.124  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 53 ms  
**Total Warnings:** 28  
**Total Errors:** 3  
**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 28

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(27)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(28)
E 252	Calc# of Seq. differs from actual; 26 seqIds defined; count=28

# SEQUENCE LISTING

<110> Albert, Lai

<120> NOVEL SPLICE VARIANTS OF HUMAN Dkk11

<130> PP023359.0003

<140> 10574182

<141> 2011-04-06

<150> PCT/US04/34256

<151> 2004-09-30

<150> 60/507682

<151> 2003-09-30

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 819

<212> DNA

<213> homo sapien

<400> 1

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<210> 2

<211> 242

<212> PRT

<213> homo sapien

<400> 2

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Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
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Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
    35           40           45
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Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu  
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 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly  
 65 70 75 80  
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly  
 85 90 95  
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Arg Thr Asp Asn  
 100 105 110  
 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln  
 115 120 125  
 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu  
 130 135 140  
 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His  
 145 150 155 160  
 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg  
 165 170 175  
 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu  
 180 185 190  
 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr  
 195 200 205  
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 agagagctcc ttgggtctca caggcctcca gagcctactc caaggcttca gccgactttt 180  
 cctgaaaggt aacctgcttc ggggcataga cagcttattc tctgccccca tggacttccg 240  
 gggcctccct gggaactacc acaaagagga gaaccaggag caccagctgg ggaacaacac 300  
 cctctccagc cacctccaga tcgacaagat gaccgacaac aagacaggag aggtgctgat 360  
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 ggtaccagag atggaggaga aggaggccct ggtaccatc cagaaggcca cggacagctt 480  
 ccacacagaa ctccatcccc ggggtggcctt ctggatcatt aagctgccac ggcggaggtc 540  
 ccaccaggat gccctggagg gcggccactg gctcagcgag aagcgacacc gcctgcaggc 600  
 catccgggat ggactccgca aggggaccca caaggacgtc ctagaagagg ggaccgagag 660  
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<210> 4  
 <211> 242  
 <212> PRT  
 <213> homo sapien

<400> 4  
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Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	Leu	Thr	Gly	Leu				
35					40					45									
Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	Lys	Gly	Asn	Leu				
50					55					60									
Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	Asp	Phe	Arg	Gly				
65					70					75					80				
Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	His	Gln	Leu	Gly				
85					90					95									
Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	Met	Thr	Asp	Asn				
100					105					110									
Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Asn	Val	Val	Ala	Ser	Ile	Gln				
115					120					125									
Pro	Ala	Glu	Gly	Ser	Phe	Glu	Gly	Asp	Leu	Lys	Val	Pro	Arg	Met	Glu				
130					135					140									
Glu	Lys	Glu	Ala	Leu	Val	Pro	Ile	Gln	Lys	Ala	Thr	Asp	Ser	Phe	His				
145					150					155					160				
Thr	Glu	Leu	His	Pro	Arg	Val	Ala	Phe	Trp	Ile	Ile	Lys	Leu	Pro	Arg				
165					170					175									
Arg	Arg	Ser	His	Gln	Asp	Ala	Leu	Glu	Gly	Gly	His	Trp	Leu	Ser	Glu				
180					185					190									
Lys	Arg	His	Arg	Leu	Gln	Ala	Ile	Arg	Asp	Gly	Leu	Arg	Lys	Gly	Thr				
195					200					205									
His	Lys	Asp	Val	Leu	Glu	Glu	Gly	Thr	Glu	Ser	Ser	Ser	His	Ser	Arg				
210					215					220									
Leu	Ser	Pro	Arg	Lys	Thr	His	Leu	Leu	Tyr	Ile	Leu	Arg	Pro	Ser	Arg				
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Gln Leu																			

<210> 5

<211> 733

<212> DNA

<213> homo sapien

<400> 5

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agagagctcc ttgggtctca caggcctcca gagcctactc caaggcttca gccgactttt 180
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cctctccagc cacctccaga tcgacaagat gaccgacaac aagacaggag aggtgctgat 360
ctccgagaat gtggtggcat ccattcaacc agcggagggg agcttcgagg gtgatttgaa 420
ggtacccagg atggaggaga aggaggccct ggtacccatc cagaaggcca cggacagctt 480
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catccgggat ggactccgca aggggaccca caaggacgtc ctagaagagg ggaccgagag 660
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<210> 6

<211> 242

<212> PRT

<213> homo sapien

<400> 6

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			20					25					30		
Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	Leu	Thr	Gly	Leu
	35					40					45				
Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	Lys	Gly	Asn	Leu
	50				55						60				
Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	Asp	Phe	Arg	Gly
65				70					75					80	
Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	His	Gln	Leu	Gly
			85						90					95	
Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	Met	Thr	Asp	Asn
	100							105					110		
Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Asn	Val	Val	Ala	Ser	Ile	Gln
	115						120					125			
Pro	Ala	Glu	Gly	Ser	Phe	Glu	Gly	Asp	Leu	Lys	Val	Pro	Arg	Met	Glu
	130					135					140				
Glu	Lys	Glu	Ala	Leu	Val	Pro	Ile	Gln	Lys	Ala	Thr	Asp	Ser	Phe	His
145				150					155						160
Thr	Glu	Leu	His	Pro	Arg	Val	Ala	Phe	Trp	Ile	Ile	Lys	Leu	Pro	Arg
			165					170					175		
Arg	Arg	Ser	His	Gln	Asp	Ala	Leu	Glu	Gly	Gly	His	Trp	Leu	Ser	Glu
	180						185				190				
Lys	Arg	His	Arg	Leu	Gln	Ala	Ile	Arg	Asp	Gly	Leu	Arg	Lys	Gly	Thr
	195					200					205				
His	Lys	Asp	Val	Leu	Glu	Glu	Gly	Thr	Glu	Ser	Ser	Ser	His	Ser	Arg
	210					215					220				
Leu	Ser	Pro	Arg	Lys	Thr	His	Leu	Leu	Tyr	Ile	Leu	Arg	Pro	Ser	Arg
225				230					235						240
Gln	Leu														

<210> 7

<211> 733

<212> DNA

<213> homo sapien

<400> 7

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gggcctccct gggaactacc acaaagagga gaaccaggag caccagctgg ggaacaacac 300
cctctccagc cacctccaga tcgacaagat gaccgacaac aagacaggag aggtgctgat 360
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ccaccaggat gccctggagg gcggccactg gctcagcgag aagcgacacc gcctgcaggc 600
catccgggat ggactccgca aggggacca caaggacgtc ctagaagagg ggaccgagag 660
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<210> 8

<211> 242

<212> PRT



<213> homo sapien

<400> 8

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Leu	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Val	Ile	Pro	Ser	Thr	Ala	Ala	Pro
			20					25					30		
Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	Leu	Thr	Gly	Leu
		35					40					45			
Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	Lys	Gly	Asn	Leu
		50					55					60			
Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	Asp	Phe	Arg	Gly
65					70					75					80
Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	His	Gln	Leu	Gly
				85					90					95	
Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	Met	Thr	Asp	Asn
			100						105					110	
Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Asn	Val	Val	Ala	Ser	Ile	Gln
		115						120						125	
Pro	Ala	Glu	Gly	Ser	Phe	Glu	Gly	Asp	Leu	Lys	Val	Pro	Arg	Met	Glu
		130					135						140		
Glu	Lys	Glu	Ala	Leu	Val	Pro	Ile	Gln	Lys	Ala	Thr	Asp	Ser	Phe	His
145					150					155					160
Thr	Glu	Leu	His	Pro	Arg	Val	Ala	Phe	Trp	Ile	Ile	Lys	Leu	Pro	Arg
				165					170					175	
Arg	Arg	Ser	His	Gln	Asp	Ala	Leu	Glu	Gly	Gly	His	Trp	Leu	Ser	Glu
			180						185					190	
Lys	Arg	His	Arg	Leu	Gln	Ala	Ile	Arg	Asp	Gly	Leu	Arg	Lys	Gly	Thr
		195					200							205	
His	Lys	Asp	Val	Leu	Glu	Glu	Gly	Thr	Glu	Ser	Ser	Ser	His	Ser	Arg
		210					215					220			
Leu	Ser	Pro	Arg	Lys	Thr	His	Leu	Leu	Tyr	Ile	Leu	Arg	Pro	Ser	Arg
225					230					235					240
Gln	Leu														

<210> 9

<211> 733

<212> DNA

<213> homo sapien

<400> 9

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agagagctcc	ttgggtctca	caggcctcca	gagcctactc	caagggttca	gccgactttt	180
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gggcctccct	gggaactacc	acaaagagga	gaaccaggag	caccagctgg	ggaacaacac	300
cctctccagc	cacctccaga	tcgacaagat	gaccgacaac	aagacaggag	aggtgctgat	360
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ggtaccagag	atggaggaga	aggaggccct	ggtaccatc	cagaaggcca	cggacagctt	480
ccacacagaa	ctccatcccc	gggtggcctt	ctggatcatt	aagctgccac	ggcggaggtc	540
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Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu  
35 40 45  
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu  
50 55 60  
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly  
65 70 75 80  
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly  
85 90 95  
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn  
100 105 110  
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln  
115 120 125  
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu  
130 135 140  
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His  
145 150 155 160  
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg  
165 170 175  
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Ser His Trp Leu Ser Glu  
180 185 190  
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr  
195 200 205  
His Lys Asp Val Leu Lys Glu Gly Thr Glu Ser Ser Ser His Ser Arg  
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Gln Leu

<210> 11  
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<212> DNA  
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ccaccaggat gccctggagg gcggccactg gctcagcgag aagcgacacc gcctgcaggc 600  
catccgggat ggactccgca aggggaccca caaggacgtc ctagaagagg ggaccgagag 660

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<210> 12

<211> 242

<212> PRT

<213> homo sapien

<400> 12

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Leu	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Val	Ile	Pro	Ser	Thr	Ala	Ala	Pro
				20				25					30		
Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	Leu	Thr	Gly	Leu
		35				40					45				
Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	Lys	Gly	Asn	Leu
		50				55					60				
Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	Asp	Phe	Arg	Gly
65					70				75					80	
Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	His	Gln	Leu	Gly
				85					90				95		
Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	Met	Thr	Asp	Asn
		100						105					110		
Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Asn	Val	Val	Ala	Ser	Ile	Gln
		115					120					125			
Pro	Ala	Glu	Gly	Ser	Phe	Glu	Gly	Asp	Leu	Lys	Val	Pro	Arg	Met	Glu